REMARKS

This Amendment responds to the Office Action dated June 26, 2002, in which the Examiner finally rejected claims 1-17 and 20, all of the claims pending in the application. In response, applicants have amended claims 1-2, 4, 9, 17, and 20. A marked version of the claims, as amended, may be found attached hereto as Exhibit A. Reexamination and reconsideration of the rejections are respectfully requested in light of the foregoing amendments and the following remarks.

The Examiner has rejected claims 1-17, and 20 under 35 U.S.C. § 112, first paragraph, as containing subject matter that allegedly was not described in the specification in such a way as to reasonably convey to one skilled in the art that the inventor at the time the application was filed, had possession of the claimed invention.

The Examiner asserts that the claims are broadly drawn to typing alleles of the minor Histocompatibility antigen HA-1 comprising detecting polymorphic nucleotides in the cDNA or genomic nucleic acids of sequence of the HA-1 antigen, or the cDNA or genomic DNA that encodes the full HA-1 antigen, but that the specification does not provide sufficient written description as to the sequence of the HA-1 antigen, or the cDNA or the genomic DNA that encodes the full HA-1 antigen.

While applicant respectfully disagrees with the Examiner's assessment, applicant has amended the claims in an effort to meet the examiner's concerns, and to advance the prosecution of the application. Thus, applicant has amended claims 1 and 2 to more clearly define the invention. The claims now refer to a region of an HA-1 allele with a sequence as shown in SEQ ID NOS 17 or 19. As shown in Figures 3 and 5, these sequences encode the HA-1 nonapeptides as shown in SEQ ID NOS 18 and 20.

As the specification makes clear, and as the Examiner concedes, applicant clearly had possession of these sequences prior to filing the present application. Further, Examples 4 and 6 show how HA-1 H and HA-1 R allele specific PCR is carried out, in order to detect polymorphic nucleotides in the cDNA or genomic nucleic acids of the alleles. Applicant submits that the Examiner's concerns about the description requirement have been overcome by the foregoing amendments.

With the amendment of claims 1 and 2, as described above, the rejections of claims 11-14 become moot. Likewise, applicant has amended claim 20 and added new claims 21 and 22 to a sequence as disclosed in the present invention, or having at least 80% homology to a sequence of the invention. Such sequences are, for example, suitable for detecting a HA-1 H or R allele region with a sequence as shown in SEQ ID NOS 17 or 19.

Finally, with respect to the rejection of claims 2, 4, 9and 17 for indefiniteness, applicant has amended claims 2,4, and 9 to refer to nucleic acid sequences only, and has amended claim 17 to remove multiple dependencies.

Applicant submits that it has addressed and overcome all of the pending rejections, and that the application is now in condition for allowance. Prompt notification to that effect is respectfully requested.

If any additional fee is required in connection with the filing of this application, authorization is hereby given to charge the amount of any such fee to the Deposit Account No. 03-3125.

Respectfully submitted,
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By _____

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I hereby certify that this paper is being deposited this date with the U.S. Postal Service as first class mail addressed to:

Assistant Commissioner of Patents,
Washington, D.C. 20231

_____ 10/28/02
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EXHIBIT A

AMENDED CLAIMS – Marked-up version

1. (Twice amended) Method for typing of alleles of the Minor Histocompatibility Antigen HA 1 in a sample, the method comprising detecting polymorphic nucleotides in the cDNA or genomic nucleic acids of said alleles, thereby typing the alleles, wherein said polymorphic nucleotides are detected in a region of said allele corresponding to SEQ ID NOS 17 or 19 in, respectively, allele HA-1 H or allele HA-1 R.

2. (Twice amended) Method [according to claim 1, further characterized in that said] for typing of alleles of the Minor Histocompatibility Antigen HA-1 [are the R allele and the H allele comprising amino acids in the sequence as shown in SEQ ID NOS: 17-20.] in a sample, the method comprising detecting polymorphic nucleotides in the cDNA or genomic nucleic acids of said alleles, thereby typing the alleles, wherein said alleles are HA-1 H or HA-1 R alleles, or a combination thereof with a sequence as shown in SEQ ID NOS 17 or 19.

4. (Twice amended) Method according to claim 1, further comprising [characterized in that]: said at least one pair of primers comprises a 5'-primer that specifically hybridizes to a target region comprising the nucleotides at position 4 or at positions 4 and 8 in the HA-1 allele, or[,] said at least one pair of primers comprises a 3'-primer that specifically hybridizes to a target region comprising the nucleotides at position 8 or at positions 4 and 8 in the HA-1 allele, with said positions being indicated in SEQ ID NOS[:17-20] 17 and 19.

9. (Twice amended) Method according to claim 7 further characterized in that said at least one probe specifically hybridizes to a target region comprising the nucleotides at position 8 or at positions 4 and/or 8 in the HA-1 allele, with said positions being indicated in SEQ ID[:17-20] 17 and 19.

13. (Amended) An isolated polynucleic acid [identified by] comprising a sequence as shown in SEQ ID NO 1, or SEQ ID NO 17 or SEQ ID NO [18] 19 or an isolated polynucleic acid displaying at least 80% [sequence] homology to said polynucleic acids, or any fragment of said polynucleic acids, that can be used as a primer or as a probe for [HA-1 typing] typing of alleles of the Minor Histocompatibility Antigen HA-1 according to claim 1.

17. (Twice Amended) A diagnostic kit for genomic typing of alleles of the Minor Histocompatibility Antigen HA-1 [according to claim 14,] with said kit comprising: a) at least one primer according to claim 10; and b) optionally, an enzyme and/or reagents enabling the amplification reaction, and/or reagents enabling the sequencing reaction.

20. (Amended) An isolated polynucleic acid [identified by SEQ ID NO. 1, or SEQ ID NO. 17, or SEQ ID NO. 18] comprising SEQ ID NO 1, or an isolated polynucleic acid displaying at least 80% sequence homology to the isolated polynucleic acid.

21. (New) An isolated polynucleic acid comprising SEQ ID NO 17, or

an isolated polynucleic acid displaying at least 80% sequence homology to the isolated polynucleic acid.

22. (New) An isolated polynucleic acid comprising SEQ ID NO 19, or an isolated polynucleic acid displaying at least 80% sequence homology to the isolated polynucleic acid.